

EXHIBIT B

>Thursday, April 28, 2005

>DNA92234 [Full]

>887 Sites [All Sites]

> [DNA92234], sheldens

> Lib309

>Sequence confirmed by phredphrap

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          thal
          nlalII  snaBI
          sphI  fnuDII/mvnI      mnlI
          nspRI  batUI  taII      taqI
          taII  nspI  bsh1236I      xhoI
          maeII/hpyCH4IV  bslVI/spII  tsp509I[M.ecoRI-]
          aluI  hnlII/acyI  cac8I  bsaAI  ecoRI  tllI
          sapi  ahaII/bsaHI  mlul  rsaI  hpy188I  smII
          mboII  aatII  cac8I  aflIII  maeII/hpyCH4IV  paeR7I  bpy188I  acII  bpmI/g
          hphI  sfoI  earI/ksp632I  hpy99I  hpyCH4V  csp6I  aluI  apoI  avaI[M.taqI-]  mnlI  fnu4HI/bsaFI  hpy18
1 TAGGTGACAC TATAGAGAG CATGACGTC GCATGCACGC GTACGTAAGC TCGGATTGG CGTCGAGGNA TGAATACCTC CGAAGCGCGT TTGTTCTCCA
ATCCACTGTG ATATCTTCTC GATCTCTGCAG CGTACGTCGCG CATGCATTGG AGCCTTAAGC CGAGCTCCTT ACTTATGGAG GCTTCGGCGA AACAAAGAGGT
^insert starts here

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GSeqEdit, DNA92234 [Full], page 1

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scrFI[M.hpaII-]
ncII
mspI
hpaII
dsvV
bpuAI bsaKI bsp1286 mnlI
bbsI bslI bsmFI taiI bmyI tru9I bphI bslI
mnlI mboII bsaJI maeII/hpyCH4IV msei maeIII nla
a'buI
101 GATGTGAATA GCTCCACTAN ACCAGCCTCG TCTTCTCTCC GGGGACACAC GTGGGTGAGG GCACAGAGAG ATATTTAAG TCACCTCTT GGGCTTTC
CTACACTTAT CGAGGTGATA TGGTCGGAGC AGAAGGAGG CCCCCTGTG CACCCAGTCC CGTGTCTCTC TATTAATTAC AGTGGAGAA CCGGAAAGT
sau3AI
mboI/ndaII(dam-)
dpnII(dam-)
dpnI(dam+)
alwI(dam-)
nlaIV
bstYI/xhoII hgaI
bamHI bslI tseI
hpy188I bstXI hpy188III fnu4HI/bsa
maeI hpaI sco57I bpmI/gsuI(dcm-) bslI auaI bbvI bsmFI
bfaI
mali
201 TGGGCTCCC TCTGCCACAT TTTTGTGAGG TTGGGAAAGT TGCTAGAGGC TTGAGACTC CAGCTTAAGT GATCCCAAC TCGGAGAGAT GGTGCTGCTC
ACCTGAGGG AGACGGTGTA AAAACCTCC AACCTTTCA AGCATCTCG AGTCTTGAG GTCGGATTAC CTAGGTTTG AGCTTCTTA CCGAGCGAGG
M D P K L G R M A A S
*NET
1

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GSeqEdit, DNA92234 [Full], page 2

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fnu4HI/bsoFI
tseI      acII
tseI      mwol      thal nlaIII      haeII
mwol      fnu4HI/bsoFI      nspHI      mspI
fnu4HI/bsoFI      fnuDI/mvnI      scrFI[M.hpalI-]
bbvI      bbvI      bstDI[M.hhaI-]      nclI
tseI      tseI      bsh1236I      dsav hinPI      bpuAI      ma
mwol      fnu4HI/bsoFI      hinPI      nspi      mwol      hpalI      bbsI      rsaI      mnlI
fnu4HI/bsoFI      hhaI/cfoI      mnlI      acII      bsaKI      xmnI      mboII      cspGI      econI
cac8I      bbvI      bpmI/gsuI[dcw-]      bseRI      mnlI      bsaJI      hhaI/cfoI      asp700      bsaI      bsaI
301 CTGCTGGCTG TGCTGCTGCT GCTGCTGGAG CGGGGCTATG TCTCTCACC CTCCCGGCC CCGGCGCTGT TAGAGAAAGT CTTCAGTAC ATTGACCTCC
GACGACCGAC ACGACGACGA CGACGACCTC GCGCGGTACA AGAGGATGG GAGGGCGGG GCGCGGACA ATCTCTTTCA GAAGTCTATG TAACTGGAGG
12 L L A V L L L L L E R G M F S S P S P P A L L E K V F Q Y I D L H

nboII
earI/ksp632I
aspI
aluI
sctI
sacI
hglAI/aspHI[M.aluI-]
ecII36II
tth111I/aspI
pleI
apoI      alwNI[dcw-]      haeII/palI      pf1FI      bsp1286[M.aluI-]
foxI tep509I      alw26I/bamAI      mscI/balI      nlyI      bslHKA I      hpy188I
bstFI      hpyCH4V      eaeI      taqI      hinFI      hpy188I      bmyI      eco57I      ea
hpy188III      bsgI      hgaI      eco57I      mnlI      eco57I      banII[M.aluI-]      cf
401 ATCAGGATGA ATTGTGCGAG ACGCTGAGG AGTGGGTCG CATCGAGAGC GACTCTGTCC AGCTGTGCC TGGCTTCAGA CAGAGCTCT TCAGATGAT
TAGTCTTACT TAAACAGTTC TCGGACTTCC TCACCCACCG GTAGCTCTCG CTGAGACAGG TGGGACACGG AGCGAGTCT GTTCTCGAGA AGTCTTACTA
46 Q D E F V Q T L K E W V A I E S D S V Q P V P R F R Q E L F R M M

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GSeqEdIt, DNA92234 [Full], page 3

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mwoI
scrFI[dcn-]
pspGI sau96I[M.haeIII-]
mvaI pspOMI/bspI20I
ecoriI[dcn-]
deaV[dcn-]
bstNI nlaIV
bskI[dcn-]
hinPI bspI286[M.haeIII-]
hhaI/cfoI sfiI
tseI bsaJI bmyI
fnu4HI/bscFI sau96I[M.haeIII-]
bbvI apyI[dcn+]
hpyCH4V banII[M.haeIII-]
sfciI haeII apaI mnlI
tseI alwNI[dcn-] haeIII/palI bsaJI
mwoI fnu4HI/bscFI pstI[M.HI-] nlaIV haeIII/palI
bceAI bbvI fnu4HI/bscFI ecoO109I/draII
haeIII/palI bbvI alw26I/bamAI bglI[M.haeIII-]
pshAI avaII alw26I/bamAI
501 GGCCTGCGCT GCGACACGC TGCAGCGCT GGGGGCCCT GTGGCTCGG TGGACATGG TCCTCAGCAG CTGCCGATG GTCAGAGCTC TCCATACCT
CCGGCACCGA CGCTGTGCG ACGTGCGCA CCGCGGCA CCGCGGCA CCTGTACC ACCTGTACC AGAGTCGT CACGGGCTAC CAGTCTCAG AGGTATGGA
79. A V A A D T L Q R L G A R V A S V D M G P Q Q L P D G Q S L P I P

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GSeqEdit, DNA92234 [Full], page 4

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    eaeI[dcn-]
    scrFI[dcn-]
    pepGI
    mvaI
    ecorII[dcn-]
    dsav[dcn-]
    bstNI bslI
    bssXI[dcn-]
    apyI[dcn+]
    foki cfrI bsrI
    bstFSI haeIII/pali
    601 CCGGTCATCC TGGCCGAAC TGGGAGCGAT CCGACGMAAG GCACCGTNG CTTCTAGCG CACTTGGAG TGCACGCTGC TGCACCGGGC GATGGGTGCG
    GGSCAGTAGG ACCGGCTTGA CCGCTCGCTA GGGTCTTTC CGTGGCAGAC GAAGATGCG GTGAACCTTC AGTGGGAGC ACTGGGCCCG CTACCCACCG
    112 P V I L A E L G S D P T K G T V C F Y G H L D V Q P A D R G D G W L

    scrFI[M.hpaII-]
    nciI
    tseI
    haeIII/pali
    bsgI cacBI
    hpaII
    dsav
    taiI bbvI
    maeII/hpyCH4IV
    bssKI
    bsaJI
    hpyCH4V
    btrI hpyCH4V
    701 TCACGACCC CTATGTCCTG ACCGAGGTAG ACCGGAACT TTATGGACGA GGAGCGACCG ACACAAAGG CCGTGTCTTG CCTTGGATCA ATGCTGTGAG
    AGTGCTGGG GATACACGAC TGCCTCCATC TGCCTTTGA ATACCTGCT CCGGCTGCT CCTGCTGCT TGTCTTTCC GGCACAGAC CGAACCTAGT TACGACACTC
    146 T D P Y V L T E V D G K L Y G R G A T D N K G P V L A W I N A V S

    sau3AI mwoI
    bslI
    sau96I[M.haeIII-] dpnII[dam-] hi
    haeIII/pali dpnI[dam+] hh
    ecoO109I/draII alwi[dam-] hae
    mnlI mcrI
    baeRI bsrI
    accI
    mnlI
    sau96I
    nlaIV
    avall
    701 TCACGACCC CTATGTCCTG ACCGAGGTAG ACCGGAACT TTATGGACGA GGAGCGACCG ACACAAAGG CCGTGTCTTG CCTTGGATCA ATGCTGTGAG
    AGTGCTGGG GATACACGAC TGCCTCCATC TGCCTTTGA ATACCTGCT CCGGCTGCT CCTGCTGCT TGTCTTTCC GGCACAGAC CGAACCTAGT TACGACACTC
    146 T D P Y V L T E V D G K L Y G R G A T D N K G P V L A W I N A V S

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GSeqEdit, DNA92234 [Full], page 5

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scrFI[dcn-]
pspGI
mvaI      sau3AI
ecorII[dcn-]
dsaV[dcn-] mboI/ndeII[dam-]
bstNI     dpnII[dam-]
bsp1286   bstXI/xhoII
bmyI bssKI[dcn-] mboII
hpy188I apyI[dcn+] dpnI[dam+]
eco57I bsaJI bglII
mwoI banII bpmI/gsuI[dcn-]
801 CGCCTTCAGA GCCCTGGAGC AGATCTTCC TGTGATATC AAATTCTATCA TTGAGGGGAT GGAAGAGGCT GGCTCTGTTC CCTGGAGGA ACTTGTGGAA
   GCGGAGTCT CGGGACCTCG TTCGAGAGG RAACTTATAG TTTAAGTAGT AACTCCCTA CCTTCTCGA CCGAGACACAC GGGACCTCT TGAACACCTT
179 A F R A L E Q D L P V N I K F I I E G M E E A G S V A L E E L V E

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mnlI
 bpmI/gsuI[dcn-]
 scrFI[dcn-]
 pspGI
 mvaI
 ecorII[dcn-]
 dsaV[dcn-]
 bstNI
 bssKI[dcn-]
 apyI[dcn+]
 bsaJI
 foki mboII cacGI
 batFSI mnlI
 null earI/ksp632I
 tep509I
 apoI
 null earI/ksp632I

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```

scrFI(
ncII
nspI
hpaII
dsv
bsaKI
bsaJI
xnaI/ps
smaI
scrFI(M
ncII
dsv
bsaKI
bsaJI
avaI(M.
nlaiV
sau3AI
mboI/ndelI(dam-)
dpmI(dam-)
dpmI(dam+)
alwI(dam-)
cac8I
bpy188I
tep509I
tsII
sau96I mboI
avaII hinfI
901 AAAGAAAGG ACCGATTCCTT CTCTGGGTGG GACTACATTS TAATTCAGA TAACCTGGG ATCAGCCAAA GGAGCCAGC ATCACTTAT GGAACCGGG
TTTCTTTTCC TGGCTAAGAA GAGACCACAC CTGATGTAC ATTAAGTCT ATTGGACACC TAGTCGGTTT CCTTCGGTGC TTATGTGATA CCTTGGGCC
212 K E K D R F F S G V D Y I V I S D N L W I S Q R K P A I T Y G T R G

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scrFI[dcm-]
pspGI
nvaI
ecorII[dcm-]
dseV[dcm-]
bstNI
bssKI[dcm-]
bsmAI
bseAI
bphI
aluI nlaIII mnlI bpyCR4V apyI[dcm+] bspCNI
          nlaIII hpy188III ddeI nlaIV
          fokI rcaI bstF5I hpy188III sfaNI bspHI
          sau3AI sap mboI/ndelI[da dpnII[dcm-] dpnI[dcm+] ea
1001 GGACAGCTA CTCATGCTG GAGGTGAAT GCAGAGACCA GGAATTTCAC TCAGGAACCT TTGGTGGCAT CCTCATGAA CCAATGGCTG ATCTGGTGC
      CCTGTGCGAT GAAGTACCCAC CTCACATTTA CGTCTCTGCT CCTAAGAGTG AGTCCTTGGG AACCCACCGTA GGAAGTACTT GGTACCCGAC TAGACCCACG
246 N S Y F M V E V K C R D Q D F H S G T F G G I L H E P M A D L V A
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GSeqEdit, DNA92234 [Full], page 8

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scriI[dcn-]
pspGI
mvaI
ecorII[dcn-]
dsaV[dcn-]
bstNI
bsaKI[dcn-]
sau96I[dcn-]
nlaIV
avaII[dcn-]
scriI[dcn-]
pspGI apyI[dcn+]
mvaI bsaFI
ecorII[dcn-]
dsaV[dcn-]
bstNI bsaJI
bsaKI[dcn-] tfII
apyI[dcn+] hinfI
mboII
1101 TCCTCTCGGT AGCCTGCTAG ACTCGTCTGG TCATATCCTG GTCCCTGGAA TCTATGATGA AGTGGTTCCT CTTACAGAG AGGAATATA TACATACAAA
AGAAAGACCA TCGAGCACATC TCGAGCACACC AGTATAGGAC CAGGACCTT AGATACACTT TCACCAGGA GAATGCTTC TCCTTATTT ATGTATGTTT
279 L L G S L V D S S G H I L V P G I Y D E V V P L T E E I N T Y K
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GSeqEdit, DNA92234 [Full], page 9

```

rsal
csp6I
nlaIV
kpnI
banI
asp718
bpml/gsuI[dcn
hpy188III
acc65I
mnlI
tflI
mnlI
bseRI
hinfI
hpyCH4V
mnlI
taqI
ddel
bseRI
hinfI
hpyCH4V
mnlI
1201 GCCATCCATC TAGACCTAGA AGRATACCGG AATAGCAGCC GGGTTCAGAA ATTCTGTTTC GATACCTAGG AGCGATTCT AATGCACCTC TGGAGGTACC
CGGTAGGTAG ATCTGGATCT TCTTATGCCC TTATGTCGG CCCACTCTT TARAGACAG CTATGATTC TCCTCTAAGA TTACGTGGAG ACCTCCATGG
312 A I H L D L E E Y R N S S R V B X F L F D T K E E I L M H L W R Y P

zmaI
maeI
rmaI
xbaI
maeI
xbaI
hpy188III
mboII
bfaI
bfaI
bseNI
hpaII
mspI
tseI
fnu4HI/bsoFI
tsp509I
apoI
bseNI
bbaI
1301 CATCTCTTTC TATTCATGGG ATCGAGGGCG CGTTTCAGA GCTGGACT AAAACAGTCA TACTGGCGG AGTTATAGGA AAATTTCAA TCCGTCTAGT
GTAGAGAAG ATAGTACCC TAGCTCCCGG GCAACTACT CGGACCTTGA TTTTGTCAGT ATGACCGGC TCANTATCCT TTTTAAAGTT AGGCAGATCA
346 S L S I H G I E G A F D E P G T K T V I P G R V I G K F S I R L V

scrFI[M.hpaII-]
ncII
mspI
hpaII
dsaV
bssXI
tseI
fnu4HI/bsoFI
tsp509I
apoI
bseNI
bbaI
1301 CATCTCTTTC TATTCATGGG ATCGAGGGCG CGTTTCAGA GCTGGACT AAAACAGTCA TACTGGCGG AGTTATAGGA AAATTTCAA TCCGTCTAGT
GTAGAGAAG ATAGTACCC TAGCTCCCGG GCAACTACT CGGACCTTGA TTTTGTCAGT ATGACCGGC TCANTATCCT TTTTAAAGTT AGGCAGATCA
346 S L S I H G I E G A F D E P G T K T V I P G R V I G K F S I R L V

haeIII/palI
eaeI[dcn-]
cfrI
acrFI[dcn-]
pspGI
mvaI
ecorII[dcn-]
dsaV[dcn-]
bstNI
bssKI[dcn-]
apyI[dcn+]
xnnI
asp700
bfaI
tsp509I
apoI
xnnI
asp700
bfaI
bam
rmaI
maeI
bfaI
1301 CATCTCTTTC TATTCATGGG ATCGAGGGCG CGTTTCAGA GCTGGACT AAAACAGTCA TACTGGCGG AGTTATAGGA AAATTTCAA TCCGTCTAGT
GTAGAGAAG ATAGTACCC TAGCTCCCGG GCAACTACT CGGACCTTGA TTTTGTCAGT ATGACCGGC TCANTATCCT TTTTAAAGTT AGGCAGATCA
346 S L S I H G I E G A F D E P G T K T V I P G R V I G K F S I R L V

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Pl      ml      hi      nlaiI      xmiI      bstXI      nlaiI
ml      maelII      hpbI      hpy188I      asp700      bstXI      nlaiI
hi      maelII      hpbI      hpy188I      asp700      bstXI      nlaiI
nlaiI      maelII      hpbI      hpy188I      asp700      bstXI      nlaiI
1401 CCCTCAGATG AATGTCGTG CGGTGGGAAA ACAGTGACA CGACACTTG AAGTGTCTT CTCGAAAGA AATAGTTCCA ACAAGATGGT TGTTCCTG
GGGAGTGTAC TTACACAGAC GCCACCTTTT TGTCCACTGT GCTGAGAC TTCTACAA GAGGTTTCT TTATCAAGGT TGTTCCTACCA ACAAGGTAC
379 P H M N V S A V E K Q V T R H L E D V F S K R N S S N K M V V S M

tspRI
sau      hpy188I
mbo      sau3AI bst4CI/hpyCH4III
dpm      mboI/ndelI[dam-]
dpm      dpmII[dam-]
alw      dpmI[dam+]
1501 ACTCTAGGAC TACACCGTG GATTCGCAAT ATTGATGACA CCGAGTATCT CGCACAAA AGAGCGATCA GAACAGTGT TGGACACGAA CCAGATATGA
TGTGATCTG ATGTGGGCAC CTAACGTTTA TAACACTGT GGTGATAGA GCGTCGTTT TCTCGCTAGT CTGTGACAAA ACCTTGCTT GGTCTATCT
412 T L G L H P N I A N I D D T Q Y L A A K R A I R T V F G T E P D M I

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GSeqEdit, DNA92234 (Full), page 11

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sau3AI
mboI/ndeII[dam-]
dpmII[dam-]
fokI dpmI[dam+]
bstE5I
scrFI[M.hpaII-]
ncII alwI[dam-]
mspI nlaIV
hpaII bstYI/xhoII
dsav bamHI
bsaKI alwI[dam-] muni/mfeI
tsp509I
1601 TCCGGGATGG ATCCACCAAT CCATTCCTCA AATGTTCCA GGAGATCCTC CACAAGAGCG TGGTCTTAAT TCCGCTGGGA GCTGTTGATG ATGGAGAAC
AGGCCCTACC TAGGTGGTAA GGTAAACGGT TTACACAGGT CCTCTAGCAG GTGTTCTGCG ACCACGATTA AGGCGACCCCT CACACACTAC TACCTCTTGT
446 R D G S T I P I A K M F Q E I V H K S V V L I P L G A V D D G E H

mspALI/nspBII
tsp509I
mmoI acII aluI
1701 TTCCGAGAT GAGAAATCA ACAGGTGGAA CTACATAGAG GGAACCAAT TATTTGTGC CTTTCTCTTA GAGATGGCCC AGCTCCATTA ATCACAAGAA
AAGGTCCTTA CTCTTTTGT TGTCCACCTT GATGTATCTC CTTGTTTAA ATAAACGACG GAAAGAAT CTCTACCGGG TCGAGGTAT TAGTGTCTT
479 S Q N E K I N R W N Y I E G T K L F A A F F L E M A Q L H O

tru9I
alNI mseI
sau96I[M.haeIII-]
haeIII/palI aseI/asnI/vspI
tseI
fnu4HI/bsaFI
ddei
nlaIV
malI
tsp509I bviI

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sau3AI
 mboI/ndelII[dam-]
 dpnII[dam-]
 dpnI[dam+]
 hpy188I
 sau3AI tspRI
 hpy188I alwI[dam-]
 hpy188I mboI/ndelII[dam-]
 rnaI mboI/ndelII[dam-] hphI
 maeI dpnII[dam-] tfilI molI foki bfai foki
 bfai dpnI[dam+] hinfI[M.hphI-] bstF3I bstF5I
 1801 CCTTCTAGTC TGATCTGATC CACTGCACAGA TTCACCTCCC CCACATCCCT AGACAGGGAT GGAATGTAAA TATCCAGAGA ATTGGGTCT AGTATAGTAC
 GGCAGATCAG ACTAGACTAG GTGACTGTCT AAGTGGAGG GGGTAGGGA TCTGTCCCTA CCTTACATTT ATAGTCTCT TAAACCCAGA TCATATCATG
 sau96I
 nlaIV
 avaII hpyCHAV
 ppuMI bseI
 eco109I/draII
 tru9I tspRI
 mseI bamFI btsI
 sau3AI
 mboI/ndelII[dam-]
 dpnII[dam-]
 dpnI[dam+]
 hpy188III
 ahallI/draI ecoRV alwI[dam-] sspI
 1901 ATTTTCCCTT CCATTAAAA TGCTTTGGGA TATCTGGATC AGTATAAAA TATTTCRAAG GCACAGATGT TGGAAANGGT TTAGGTCCC CCACCTGCACA
 TAAAGGGAA GGTAATTTT ACAGAACCTT ATAGACCTAG TCATTTTIT ATRAAGTTT CGTCTCTACA ACCTTTACCA AATTCACGGG GGTGACCTGT

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CGSeqEdit, DNA92234 [Full], page 14

```

scrFI[M.hpaII-]
ncII
mspI
hpaII
dsav
bsaKI      sau96I rsaI
xmaI/pspAI  rsrII/cspI
smaI      mroI   plaIV
acII      scrFI[M.hpaII-] cpoI kpnI hpyCH4V
fnu4HI/bsoFI      taqI ncII      hpy188III csp6I
haeIII/paII      sstI salI dsav      bspMI banI sfcI
mcrI      sacI hincII/hindII[M.taqI-] avaiI[M.hpaII-]
eagI/xmaIII/ecI XI aluI accI[M.taqI-] trn9I mspI asp718
eaeI      hgaI/aspHI[M.aluI-] mseI bspEI cfr10I/bsaFI
cfrI      rnaI      eci136II      bseKI aseI/asnI/vspI acc65I cac8I
bsIEI      maeI      bsp1286[M.aluI-] xmnI tsp509I bsaWI pstI
notI      bfaI      bsiHKAI      bsaJI tsp509I bsaWI ageI sse8387I
fnu4HI/bsoFI      bmyI hpy99I avaiI[M.hpaII-] hpaII mspI bspMI
acII      speI      banII[M.aluI-] asp700 accIII hpaII sbfI csp6I aluI sf
2301 AAAAAAAAAA AAAGGGGGC CGCGGACTAG TGAGCTGCTC GAACCGGGA TTAATTCGG ACCGGTACCT GCAGCGGTAC CAGCTTTCCC
TTTTTTTTT TTTTTTTTT TTTCCCGCCG CGGCTGATC ACTCGGCAG CTGGGCCCTT AATTAAGGCC TGCCATGGA CGTCGCCATG GTCGAAGGG
pleI
mlyI
hinfI      aluI
2401 TATAGTGAGT CGTATTAGAG CTTCG
ATATCACTCA GCATAATCTC GAACC

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GSeqEdit, DNA92234 [Full], page 15

> length: 2425

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aatII (GACGTC) :
acc65I (GGTACC) :
accI (GTAKAC) :
accIII (TCCGGA) :
aciI (CGGC) :
acyI (GRCGYC) :
afiIII (ACRYGT) :
ageI (ACCGGT) :
ahaII (GRCGYC) :
ahalII (TTTAAA) :
albi (AGCT) :
alw26I (CAGNNCTG) :
alwI (GGATCNNN) :
alwNI (CAGNNCTG) :
apaI (GGGCCC) :
apoI (RAATY) :
apyI (CCWGG) :
asoI (ATTAAAT) :
asnI (ATTAAT) :
asp700 (CAANNNTTC) :
asp718 (GGTACC) :
asphi (GWGCHC) :
aspI (GACNNNGTC) :
avaI (CYCGNG) :
avaII (GGWCC) :
bali (TGGCCA) :
bamHI (GGATCC) :
banI (GGYRCC) :

25
1295 2374
727 1117 2348
2366
86 332 355 511 1420 1672 2326 2330
25
37
2371
25
1914
19 48 110 485 569 1006 1680 1781 2016 2343 2392 2419
418 523 565
270 271 628 785 959 1319 1599 1609 1610 1817 1936
418 523 565
533
54 409 841 1249 1381 1879
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
1787 2219 2360
1787 2219 2360
375 1159 1379 1469 2358
1295 2374
484 2152 2342
451
62 280 995 2353
559 705 909 1140 1985 2143 2369
437
270 1609
640 1295 2374

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banII (GRCGYC) : 484 533 809 2342
bbsI (GAAGACNNNNNN) : 130 379 587
bbvI (GCAGC) : 292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
bceAI (ACGGCNNNNNNNNNN) : 502 656
bfaI (CTAG) : 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
bglI (GCCNNNNNGGC) : 535
bglII (AGATCT) : 822
bmyI (GDGCHC) : 159 484 533 809 2152 2342
bpmI (CTGGAG) : 96 258 325 814 883 1290
bpuAI (GAAGACNNNNNN) : 130 379 587
bsaAI (YACGTR) : 42
bsaHI (GRCGYC) : 25
bsaI (GGTCNNNNNN) : 1034 2234
bsaJI (CCNNGG) : 139 359 503 528 545 684 812 881 995 996 1143 1516 2060 2353
bsaWI (WCCGGW) : 1226 2127 2366 2371
bseRI (GAGGAGNNNNNNNN) : 342 749 1270
bsgI (GTGCAG) : 415 670 1994
bsh1236I (CGCG) : 38 331 1329
bsjEI (CGRYCG) : 755 2327
bsjHKAI (GWGWC) : 484 2152 2342
bsjWI (CGTACG) : 40
bsjI (CCNNNNNNNGG) : 135 184 274 275 354 396 614 631 771 1847 1848 2060
bsmAI (GTCTC) : 1034 2235
bsmAI (GTCTC) : 1034 2235
bsmFI (GGGACNNNNNNNNNNNN) : 143 202 297 1141 1399 1986
bsOFI (GCNGC) : 85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756
2017 2024 2326 2329
bsp120I (GGGCC) : 533
bsp1286 (GDGCHC) : 159 484 533 809 2152 2342
bspCNI (CTCAGNNNNNNNN) : 563 1050
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bspEI (TCCGA) : 2366
bspHI (TCATGA) : 1074
bspMI (ACCTGC) : 2377
bspMI (TCCGA) : 2366
bbrFI (RCCGGY) : 2371
384 618 1542
bbrI (ACTGGN) : 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
bssKI (CCNGG) : 1363 1602 1638 2061 2353 2354
2155
643 1354 1573
641
503 1516
405 606 857 1068 1203 1605 1844 1857 2175
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
38 331 1329
260 1478
270 822 1609
503 1516
667
1992
31 35 303 675 868 975 2020 2381
330 364 525 800 1328
2371
437 500 611 657 1365 2327
2368
41 387 1296 1897 2375 2387
2368
563 1050 1265 1767
271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
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dpnII (GATC) :
271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
draI (TTTAAA) :
1914
draII (RGNCCY) :
532 558 768 1984 2142
642
draIII (CACNNGTG) :
503 1516
dsaI (CCRYGG) :
139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
1363 1602 1638 2061 2353 2354
dsav (CCNGG) :
437 500 611 657 1365 2327
2327
eaeI (YGGCCR) :
15 487 862 1100 1177
eagI (CGGCCG) :
484 2342
earI (CTCTTCNNNN) :
2327
ec1136II (GAGCTC) :
250 424 474 489 804
396
ec1XI (CGGCCG) :
532 558 768 1984 2142
54
eco57I (CTGAAG) :
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
1929
ecoNI (CCTNNNNNAGG) :
85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756
2017 2024 2326 2329
ecoO109I (RGNCCY) :
38 331 1329
ecorI (GAATTC) :
405 606 857 1068 1203 1605 1844 1857 2175
ecorII (CCWGG) :
96 258 325 814 883 1290
ecorV (GATATC) :
363 524 799
fnu4HI (GCNGC) :
438 501 534 543 612 658 769 1366 1776 2328
295 420
fnuDII (CCGG) :
484 2152 2342
fokI (GGATG) :
330 364 525 800 1328
gslI (CTGGAG) :
330 364 525 800 1328
haeII (RGCGCY) :
gseI (GACGCG) :
hgiAI (GAGCAG) :
hhaI (CCGC) :
hlnPI (CCGC) :

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hincII (GTYRAC) : 2348
hindII (GTYRAC) : 2348
hinfI (GATC) : 204 451 585 914 1120 1148 1275 1500 1829 2070 2407
25
139 361 684 996 1227 1239 1602 2128 2354 2367 2372
3 181 346 1023 1434 1832
51 79 252 476 491 582 806 946 1568 1809 1814
97 281 402 443 1051 1074 1209 1289 1446 1873 1933 2156 2366
27 2347
643 1354 1573
26 43 149 668
34 416 521 671 1030 1283 1524 1995 2023 2051 2104 2380
1295 2374
15 487 862 1100 1177
243 1210 1216 1396 1504 1805 1849 1889 2140 2337
26 43 149 668
4 180 1435 2158
271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
15 131 380 488 588 825 862 917 1101 1177 1219 1450
755 2327
1622
37
204 451 585 1120 1500 2407
65 77 126 185 209 227 246 344 350 396 469 545 562 598 724 749 853
865 886 1021 1168 1180 1270 1287 1293 1324 1402 1738 1835 2005 2146
2366
437
175 1788 1915 1981 2220 2361
400 1405 1407
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hincII (GTYRAC) :
hindII (GTYRAC) :
hinfI (GATC) :
hnlI (GACGTC) :
hpaII (CCGG) :
hphI (GGTGA) :
hpy188I (TCNGA) :
hpy188III (TCNNGA) :
hpy99I (CGWCG) :
hpyCH4III (ACNGT) :
hpyCH4IV (ACGT) :
hpyCH4V (TGCA) :
kpnI (GSTRACC) :
ksp632I (CTCTTCNNNN) :
maeI (CTAG) :
mseII (ACGT) :
maeIII (GTNAC) :
mboI (GATC) :

mboII (GAGCA) :
mcrI (CGRYCG) :
mfeI (CAATTG) :
mluI (ACCGGT) :
mlyI (GAGTCNNNN) :
nmlI (CCTC) :

nroI (TCCGGA) :
nscI (TGGCGA) :
mseI (TTAA) :
mblI (CAYNNNRGTG) :

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mspAI(CMGCKG):
mspI(CCGG):
munI(CAATTG):
mvaI(CCWGG):
mvnI(CGCG):
mwol(GCNNNNNGC):
ncII(CCSGG):
ndeI(GATC):

nlaIII(CATG):
nlaIV(GGNCC):
notI(GCGGCCGC):
nspBII(CMGCKG):
nspHI(RCATGY):
nspI(RCATGY):
paerVI(CTCGAG):
pali(GGCC):
pfIFI(GACNNNGTC):
pleI(GAGTCNNN):
ppuMI(RGGWCCY):
pshAI(GACNNNGTC):
pspAI(CCCGGG):
pspGI(CCWGG):
pspOMI(GGGCCC):
pstI(CTGCAG):
pvuII(CAGCTG):
rcal(TCATGA):
rmaI(CTAG):
rsaI(GTAC):
rarII(CGGWCCG):

568 1672
139 361 684 996 1227 1239 1602 2128 2354 2367 2372
1522
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
38 331 1329
303 312 315 321 357 502 535 641 650 793 802 1555 1665
139 360 684 995 996 1239 1602 2353 2354
271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
2183
32 199 336 555 1014 1075 1315 1407 1497
270 532 533 558 640 705 991 1054 1140 1164 1295 1609 1741 1985 2374
2326
568 1672
31 335
31 335
62
438 501 534 543 612 658 769 1366 1776 2328
451
204 451 585 1120 1500 2407
558 1984 2142
553
995 2353
528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
533
520 2379
568
1074
243 1210 1216 1396 1504 1805 1849 1889 2140 2337
41 387 1296 1897 2375 2387
2368
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sacI (GAGCTC): 484 2342
 balI (GTCGAC): 2348
 sapI (GCTCTTCNNNN): 15 486 1099
 sau3AI (GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
 2183
 sau56I (GNNCC): 533 534 559 705 769 909 1140 1776 1985 2143 2369
 sbfI (CCGCGAG): 2378
 scrFI (CCNGG): 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
 1363 1602 1638 2061 2353 2354
 1067
 sfaNI (GCATC): 10 520 2379 2400
 bfcI (CTRYAG): 534
 sfiI (GGCCNNNNNGGCC): 995 2353
 smaI (CCCGGG): 62 2006 2147
 smlI (CTYRAG): 42
 snaBI (TACGTA): 2336
 apeI (ACTAGT): 31
 sphI (GCATGC): 40
 eplI (CGTACG): 2378
 sse8387I (CCTGCAGG): 1528 1949
 sspI (AATATT): 484 2342
 satI (GAGCTC): 26 43 149 668
 taiI (ACGT): 63 443 1259 1322 2349
 taqI (TCGA): 914 1148 1275 1829 2070
 tflI (GAWTC): 38 331 1329
 thaI (CCGG): 62
 tliI (CTCGAG): 175 1788 1915 1981 2220 2361
 tru9I (TTAA): 292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
 tseI (GCWGC): 4 180 1435 2158
 tsp45I (GTSAC): 55 410 842 942 1250 1382 1623 1668 1748 1880 2107 2359 2363
 tsp509I (AATT):

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